

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_2n.mph

Run on: January 16 2003, 17:00:17 : Search time 54.4 Seconds
(without alignments)
114.746 Million cell updates/sec

Title: US-09-856-070-17

Perfect score: 69
Sequence: 1 EREEQMMPEEEL 14

Scoring table:

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Ygapop 10 0	Ygapext 0 5
Egapop 6 0	Egapext 7 0
Delop 6 0	Del-ext 7 0

Searched: 393868 seqs, 22293444 residues

Total number of hits satisfying chosen parameters: 747736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB-PublishedApplications_NA -QMI-fastap -SUFFIX-rnpb -MINMATCH=0.1
-LOCPCL=0 -LPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-Elosumb2
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=10 -THRESH=1 -XGAPOP=10 -XGAPEXT=0.5 -EGAPOP=6
-EGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=7

Database: published Applications_NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	100.0	2930	US 09 960-253-156	Sequence 156, App
2	69	100.0	3044	US-09-864-864-129	Sequence 3718, App
3	69	100.0	4047	US-09-864-864-129	Sequence 324, App
4	69	100.0	4115	US-09-925-299-123	Sequence 123, App

51	73.9	2170	9	US-09-854-133-728	Sequence 728, App
47	68.1	1831	10	US-09-764-864-120	Sequence 620, App
47	68.1	2054	10	US-09-764-864-185	Sequence 185, App
8	68.1	2954	9	US-10-928-072-15	Sequence 15, Appli
46	68.7	2237	9	US-10-928-072-15	Sequence 45, Appli
45	68.2	234	10	US-09-474-650-3611	Sequence 3611, Ap
45	65.2	3257	9	US-09-764-864-264	Sequence 264, Appli
12	65.2	8055	9	US-09-858-546-3	Sequence 3, Appli
44	64.8	303	10	US-09-764-846-290	Sequence 290, App
44	64.8	404	10	US-09-764-846-290	Sequence 291, App
44	64.8	524	10	US-09-924-035A-338	Sequence 338, App
44	64.8	600	10	US-09-864-761-7218	Sequence 7218, Ap
43	62.3	265	10	US-09-764-864-753	Sequence 753, App
43	62.3	300	10	US-09-864-761-32122	Sequence 32122, A
43	62.3	365	10	US-09-764-864-338	Sequence 338, App
43	62.3	523	10	US-09-864-761-15814	Sequence 15814, A
43	62.3	4108	10	US-09-925-301-493	Sequence 493, App
42	60.9	94	10	US-09-925-301-493	Sequence 167, App
42	60.9	128	9	US-09-754-853A-186	Sequence 186, App
42	60.9	210	10	US-09-867-701-9367	Sequence 9367, Ap
42	60.9	235	10	US-09-867-701-8942	Sequence 8942, Ap
42	60.9	403	10	US-09-772-1314-7	Sequence 7, Appli
42	60.9	1155	10	US-09-822-849A-193	Sequence 193, App
42	60.9	1533	10	US-09-917-800A-1595	Sequence 1505, Ap
42	60.9	3240	10	US-09-764-864-2314	Sequence 2314, Ap
42	60.9	513004	4	US-09-754-853A-4	Sequence 4, Appli
41	59.4	456	10	US-09-864-761-13986	Sequence 13986, A
41	59.4	501	10	US-09-954-456-1458	Sequence 1458, Ap
41	59.4	553	10	US-09-864-761-30549	Sequence 30549, A
41	59.4	743	10	US-09-770-149-44	Sequence 44, Appli
41	59.4	985	10	US-09-770-149-44	Sequence 265, App
41	59.4	1282	4	US-09-938-842A-4552	Sequence 4552, Ap
41	59.4	2000	9	US-09-938-842A-4945	Sequence 4925, Ap
41	59.4	2167	9	US-10-928-072-159	Sequence 159, App
41	59.4	2264	10	US-09-863-299-1	Sequence 1, Appli
41	59.4	2785	10	US-09-925-301-122	Sequence 122, App
41	59.4	37093	10	US-09-768-781-5	Sequence 5, Appli
41	59.4	20556	10	US-09-880-107-3945	Sequence 3945, Ap
41	59.4	42999	10	US-09-740-029-3	Sequence 3, Appli
41	59.4	397658	10	US-09-813-120-3	Sequence 3, Appli
40	58.0	92	10	US-09-864-761-21177	Sequence 21177, A

ALIGNMENTS

RESULT 1 US 09 960-253-156
US 09 960-253-156 Affected by US 09 960-253-156
Parent No. US0909313619A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Mohamath, Raouh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF LUNG CANCER
FILE REFERENCE: 210121.556
CURRENT APPLICATION NUMBER: US/09/960.253
CURRENT FILING DATE: 2001 09 20
NUMBER OF SEQ ID NOS: 187
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 156
LENGTH: 2930
TYPE: DNA
ORGANISM: Homo sapiens
US-09-960-253-156

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Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
Mismatches:	0
Indels:	0
Gaps:	0

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US 09-856-070-17 (1-14) x US-09-960-253-156 (1-2930)

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DB 1076 GAGACAGAGAAAGACATGATGATGATGATGATGATGATGATG 1117

RESULT 2
US 09-880-107-3718
: Sequence 3718, Application US/09880107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
: APPLICANT: Horne, Daniel L.
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Scherl, Iwe
: APPLICANT: Gene Logic, Inc.
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880-107
: PRIOR FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3718
: LENGTH: 4044
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURES:
: OTHER INFORMATION: Genbank Accession No. US20020142981A1 X51521
: NAME/KEY: unsure
: LOCATION: (1)-(4044)
: OTHER INFORMATION: n - a or c or q or t
US 09-880-107-3718

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Pred. No.: 0.00372 Length: 4044
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US 09-856-070-17 (1-14) x US-09-880-107-3718 (1-4044)

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DB 1117 GAGACAGAGAAAGACATGATGATGATGATGATGATGATGATG 1158

RESULT 3
US 09-864-864-329
: Sequence 329, Application US/09864864
: Patent No. US20020102679A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Dillon, David G.
: APPLICANT: Secrist, Heather
: APPLICANT: Lodes, Michael J.
: APPLICANT: Alqate, Paul A.
: APPLICANT: Flind, Steve P.
: APPLICANT: Mannion, Jane
: APPLICANT: Benson, Darin R.
: APPLICANT: Carter, Patrick
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121-524
: CURRENT APPLICATION NUMBER: US/09/864-864
: CURRENT FILING DATE: 2001-05-23
: NUMBER OF SEQ ID NOS: 141

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: SOFTWARE: Corixa Invention Disclosure Database
: SEQ ID NO 329
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: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)-(3047)
: OTHER INFORMATION: n - A,T,C or G
US-09-864-864-329

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US-09-856-070-17 (1-14) x US-09-864-864-329 (1-3047)

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RESULT 4
US-09-925-299-123
: Sequence 123, Application US/09925299
: Patent No. US20020055627A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA102
: CURRENT APPLICATION NUMBER: US/09/925-299
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCI/0500/05883
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1556
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 123
: LENGTH: 3115
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-925-299-123

Alignment Scores:
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US-09-856-070-17 (1-14) x US-09-925-299-123 (1-3115)

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DB 1149 GAGACAGAGAAAGACATGATGATGATGATGATGATGATGATG 1190

RESULT 5
US-09-854-133-728
: Sequence 728, Application US/09854133
: Publication No. US20020183499A1
: GENERAL INFORMATION:
: APPLICANT: Lodes, Michael J.
: APPLICANT: Mohamath, Raodoh
: APPLICANT: Henderson, Robert A.
: APPLICANT: Benson, Darin R.
: APPLICANT: Secrist, Heather
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
: TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER

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PRIOR FILING DATE: 1997-11-17	
PRIOR APPLICATION NUMBER: 60/066364	
PRIOR FILING DATE: 1997-11-21	
PRIOR APPLICATION NUMBER: 60/066453	
PRIOR FILING DATE: 1997-11-24	
PRIOR APPLICATION NUMBER: 60/066511	
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PRIOR APPLICATION NUMBER: 60/069494	
PRIOR FILING DATE: 1997-12-16	
PRIOR APPLICATION NUMBER: 60/072320	
PRIOR FILING DATE: 1998-01-23	
PRIOR APPLICATION NUMBER: 60/073612	
PRIOR FILING DATE: 1998-02-01	

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: PRIOR FILING DATE: 1998-06-18
: PRIOR APPLICATION NUMBER: 60/089947
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: 60/090349
: PRIOR FILING DATE: 1998-06-23
: PRIOR APPLICATION NUMBER: 60/090429
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090445
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090538
: PRIOR FILING DATE: 1998-06-24
: PRIOR APPLICATION NUMBER: 60/090863
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: 60/091360
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091519
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091982
: PRIOR FILING DATE: 1998-07-07

Alignment Scores:
Pred. No.:      22.7      Length:      2237
Score:          46.00     Matches:      8
Percent Similarity: 85.71% Conservative:    4
Best Local Similarity: 57.14% Mismatches:    2
Query Match:      66.67% Indels:      0
DB:              9      Gaps:      0

US-09-856-070-17 (1-14) x US-10-028-072 45 (1-2237)

Qy      1  GluA9GluLysGluGlnMetMetAraGluLysGluGluLeu 14
Db      1885  CAAAGCGCAACAGGAGCAATGATGCGACGAGGGAGAGATC 1926

RESULT 10
US-09-974-300-3611
: Sequence 3611, Application US/09974300
: Patent No. US2002014672A1
: GENERAL INFORMATION:
: APPLICANT: Herka, Randy M.
: APPLICANT: Klausen, Ib Groth
: TITLE OF INVENTION: Methods For Monitoring Multiple Genes
: TITLE OF INVENTION: Expression
: FILE REFERENCE: 10085,500-US
: CURRENT APPLICATION NUMBER: US/09/974,300
: CURRENT FILING DATE: 2001-10-05
: PRIOR APPLICATION NUMBER: 09/680,598
: PRIOR FILING DATE: 2000-10-06
: PRIOR APPLICATION NUMBER: 60/279,526
: PRIOR FILING DATE: 2001-03-27
: NUMBER OF SEQ IDS NCS: 8481
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3611
: LENGTH: 234
: TYPE: DNA
: ORGANISM: Bacillus licheniformis
US-09-974-300-3611

Alignment Scores:
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Percent Similarity: 100.00% Conservative:    6
Best Local Similarity: 53.85% Mismatches:    0
Query Match:      65.22% Indels:      0
DB:              10      Gaps:      0

US-09-856-070-17 (1-14) x US-09-974-300-3611 (1-234)

Qy      1  GluA9GluLysGluGlnMetMetAraGluLysGluGluLeu 13
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RESULT 11

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; Patent No. US20020102638A1
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; GENERAL INFORMATION:
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; APPLICANT: ROSCO et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed. Serial FAIM of file dropped
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 290
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-846-290

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Alignment Scores:	5.38	Length:	303
Pred. No.:	44.00	Matches:	8
Score:	78.57%	Conservative:	3
Percent Similarity:	77.14%	Mismatches:	3
Best local Similarity:	63.77%	Indels:	0
Query Match:	100%	Gaps:	0

1000

; sequence 231, Application 03/03,048-0
; Patent No. US20020102638A1

Search completed: January 16, 2003, 21:46:02
Job time : 62.4 secs